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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: Wed May 02 10:33:27 EDT 2007

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Application No:10579290

Version No:1.0

Input Set:

Output Set:

Started:2007-04-25 14:21:40.909

Finished:2007-04-25 14:21:40.978

Elapsed:0 hr(s) 0 min(s) 0 sec(s) 69 ms

Total Warnings:0

Total Errors:0

No. of SeqIDs Defined:4

Actual SeqID Count:4

ErrCode	Error Description
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<110> OncoMab GmbH
VOLLMER, Heinz
MULLER-HERMELINK, Hans-Konrad

<120> Human monoclonal antibody

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<150> 10/579,290
<151> 2004-11-12

<150> EP - 03 026 161.4
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Gln Thr Ala Ser Ile Thr Cys Ser Gly Asp Lys Leu Gly Asp Lys
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Tyr Ala Cys Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val Leu
35 40 45

Val Ile Tyr Gln Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg
50 55 60

Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser
65 70 75

Gly Thr Gln Ala Met Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp
80 85 90

Asp Ser Ser Ile Val Val
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Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly
1 5 10 15

cag aca gcc agc atc acc tgc tct gga gat aaa ttg ggg gat aaa 90
Gln Thr Ala Ser Ile Thr Cys Ser Gly Asp Lys Leu Gly Asp Lys
20 25 30

tat gct tgc tgg tat cag cag aag cca ggc cag tcc cct gtg ctg 135
Tyr Ala Cys Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val Leu
35 40 45

gtc atc tat caa gat agc aag cgg ccc tca ggg atc cct gag cga 180
Val Ile Tyr Gln Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg
50 55 60

ttc tct ggc tcc aac tct ggg aac aca gcc act ctg acc atc agc 225
Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser
65 70 75

ggg acc cag gct atg gat gag gct gac tat tac tgt cag gcg tgg 270
Gly Thr Gln Ala Met Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp
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gac agc agc att gtg gta
Asp Ser Ser Ile Val Val
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<210> 3
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Arg	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser
				20					25					30

Ser	Tyr	Ala	Met	His	Trp	Val	Arg	Glu	Ala	Pro	Gly	Lys	Gly	Leu
				35					40					45

Glu	Trp	Val	Ala	Val	Ile	Ser	Tyr	Asp	Gly	Ser	Asn	Lys	Tyr	Tyr
				50					55					60

Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser
				65					70					75

Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp
				80					85					90

Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Asp	Arg	Leu	Ala	Val	Ala	Gly
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Lys	Thr	Phe	Asp	Tyr
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Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly
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Arg	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	
				20					25					30	

agc tat gct atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg 135
 Ser Tyr Ala Met His Trp Val Arg Glu Ala Pro Gly Lys Gly Leu
 35 40 45

gag tgg gtg gca gtt ata tca tat gat gga agc aat aaa tac tac 180
Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr
50 55 60

gca gac tcc gtg aag ggc cga ttc acc atc tcc aga gac aat tcc 225
Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
65 70 75

aag aac acg ctg tat ctg caa atg aac agc ctg aga gct gag gac 270
Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
80 85 90

acg gct gtg tat tac tgt gcg aga gat cgg tta gca gtg gct ggt 315
Thr Ala Val Tyr Tyr Cys Ala Arg Asp Arg Leu Ala Val Ala Gly
95 100 105

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aaa act ttt gac tac                                     330
Lys Thr Phe Asp Tyr
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